

REMARKS

Claims 1-57 are cancelled. Claims 58-61 are amended. Claims 58-70 are pending. Support for the amendments can be found in the specification as originally filed, particularly at page 23, lines 13-22.

Attorney Docket Number

Please change the docket number from “BB-1270” to “2119-4273 (BB-1270)”.

Sequence Listing

In response to the Examiner’s request for clarification of the sequence listing, nucleotides 204 to 2348 of SEQ ID NO:9 encode the 715 amino acid sequence of SEQ ID NO:10.

35 USC § 112, second paragraph

Claims 58-70 are rejected under 35 U.S.C. § 112, second paragraph, as being indefinite due to the phrase “Clustal V method of alignment” (Office Action, page 2, paragraph 4). Applicants respectfully traverse. However, in order to advance prosecution, the claims are amended as suggested by the Examiner to clarify the alignment method and as disclosed on page 23 of the specification. Withdrawal of the rejection is requested.

Scope of Enablement

Claims 58-61 and 64-70 are rejected under 35 U.S.C. § 112, first paragraph, scope of enablement. Applicants respectfully traverse.

The Examiner concedes that the specification is enabling for SEQ ID NO:9 or a polynucleotide encoding SEQ ID NO:10. However, the Examiner asserts that claims reciting less than 100% sequence identity “are not enabled because they encompass unspecified base deletions, additions, substitutions, and combinations thereof while retaining enzymatic activity,” (Office Action, page 3, paragraph 5). The Examiner states that “further guidance is necessary as to what changes would be tolerated,” (Office Action, page 3, paragraph 5).

In response, Applicants direct the Examiner’s attention to Day et al, *Biochimica et Biophysica Acta*, 1998, 1399: 219-224. The reference discloses two highly conserved motifs among aminoacyl-tRNA synthetases, the “HIGH” motif and the “LSKRK” motif. The former is the putative ATP binding site and the latter the putative binding site of the 3’ end of the tRNA. Attached hereto as Appendix A is a comparison of SEQ ID NO:10 of the pending claims with the Glu-tRNA synthetase sequence from *Arabidopsis* (NCBI GI No. 3435196) disclosed by Day et al. Both sequences show substantial sequence homology in addition to the two highly conserved sequence motifs. One skilled in the art would appreciate that the more highly conserved a residue is, the less likely that it could be modified while maintaining function. From the alignment presented, and the domains illustrated in the attached Appendix A, one could quickly determine which amino acid residues might be modified in SEQ ID NO:10 without a likely change in function. Since SEQ ID NO:10 and the *Arabidopsis* sequence share only 67% identity, one of skill in the art would have appreciated that many variants sharing at least 80% sequence identity to the SEQ ID NO:10 would be expected to retain Glutamyl-tRNA synthetase activity.

In view of the discussion above, Applicants believe sufficient guidance is provided to one skilled in the art to make and use the claimed invention commensurate in scope with the claims without undue experimentation.

Written Description

Claims 58-61 and 64-70 are rejected under 35 U.S.C. § 112, first paragraph, written description. Applicants respectfully traverse.

The Examiner asserts that the claims encompass mutants and allelic variants, and that the Applicants do not disclose a representative number of species as encompassed by the claims (Office Action, page 4, paragraph 6). The Examiner further asserts that there is insufficient relevant identifying characteristics to allow one skilled in the art to predictably determine such mutants, allelic variants and Glutamyl-tRNA synthetases from other plants and organisms, absent further guidance (Office Action, page 4, paragraph 6).

In response, the Examiner's attention is directed to the specification at page 8, line 25 to page 10, line 3, which rather than disclosing a single polynucleotide encoding SEQ ID NO:10, in fact discloses alterations in the nucleotide sequence that are not expected to alter functionality, such as alterations that produce a chemically equivalent amino acid at a given site, or alterations in the N- or C-terminus portions. Thus, the skilled artisan would immediately understand the specification to disclose a representative number of polynucleotide sequences, having different nucleotide substitutions, that encode Glutamyl-tRNA synthetase, but that vary (within 80% sequence identity) from SEQ ID NO:10.

Therefore, sufficient relevant identifying characteristics have been disclosed to allow one skilled in the art to predictably determine mutants, allelic variants, and Glutamyl-tRNA synthetases from other plants and organisms.

CONCLUSION

Based on the foregoing amendments and remarks, Applicants respectfully request reconsideration and withdrawal of the rejection of claims and allowance of this application.

AUTHORIZATION

The Commissioner is hereby authorized to charge any additional fees which may be required for consideration of this Amendment to Deposit Account No. 13-4500, Order No. 2119-4273. A DUPLICATE OF THIS DOCUMENT IS ATTACHED.

In the event that an extension of time is required, or which may be required in addition to that requested in a petition for an extension of time, the Commissioner is requested to grant a petition for that extension of time which is required to make this response timely and is hereby authorized to charge any fee for such an extension of time or credit any overpayment for an extension of time to Deposit Account No. 13-4500, Order No. 2119-4273. A DUPLICATE OF THIS DOCUMENT IS ATTACHED.

Respectfully submitted,
MORGAN & FINNEGAN, L.L.P.

Dated: August 13, 2004

By:


Michael A. Willis
Registration No. 53,913
(212) 415-8700 Telephone
(212) 415-8701 Facsimile

Correspondence Address:

MORGAN & FINNEGAN, L.L.P.
3 World Financial Center
New York, NY 10281-2101

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Appendix A shows a comparison of the amino acid sequences of the glutamyl-tRNA synthetase proteins from corn (SEQ ID NO:10) and Arabidopsis (NCBI gi: 3435196). Amino acids conserved among both sequences are indicated with an asterisk (*) on the top row; dashes are used by the program to maximize alignment of the sequences. Two conserved motifs are underlined (Day et al., 1998, BBA 1399: 219-224).

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*      ***      *** * * *      *      * **      *      *      *      *      *
SEQ ID NO:10 MEAA-LSFSKDSPPISIICAALKVLGPLTINHSLAAGSAPTLQFASGESLHGVNPIILYI
GI:3435196 MDGMKLSFPPEPPLSVIVALSLSASPVTIDSSAAATTVPSFVFSGDKLNGATVLLRYV

*      *      *      *      *      *      *      *      *      *      *      *      *
SEQ ID NO:10 ARGAS-IASLSGKNDIEFGHVVEWLEYAPTFLSGSEFENAACLFDVGLASRTFLVGHGLT
GI:3435196 GRSAKKLPDFYGNNAFDSSQIDEWVDYASVFFSGSEFENACGRVDKYLESTFLVGHSL

***      *      *      *      *      *      *      *      *      *      *      *      *
SEQ ID NO:10 IADIAVWSNLAGIGQRWESLRSKKYQNLVRWFNSIDSEYKEALNEVVAFGVKRGIGKS
GI:3435196 IADVAIWSALAGTGQRWESLRSKKYQSLVRWFNSILDEYSEVLNKVLATYV-KKGSGKP

*      *      *      *      *      *      *      *      *      *      *      *      *
SEQ ID NO:10 -PAPSLKEKVKH---DSKDPSAPEVDLPGAKVGKVCVRFAPEPSGYLHIGHAKAALLNKY
GI:3435196 VAAPKSKDSQQAVKGDGQDKGKPEVDLPEAEIGVKLRFAPEPSGYLHIGHAKAALLNKY

*****      *****      *****      *      *      *      *      *      *      *      *
SEQ ID NO:10 FAERYQGRLIVRFDDTNPSKESNEFVENLLKDIETLGKTYDAVITYTSDYFPKLMEMAESL
GI:3435196 FAERYQGEVIVRFDDTNPAKESNEFVDNLVKDIGTLGKTYEKVITYTSDYFPELMDMAEKL

*****      *****      *      *      *      *      *      *      *      *      *      *
SEQ ID NO:10 IKQGKAYIDDTPKEQMRKERMDGIESRCRNNTVEENLSLWKEVNTERGMQCCVRGKLD
GI:3435196 MREGKAYVDDTPREQMOKERMDGIDSKCRNHSVEENLKLWKEAGSERGLQCCVRGKFN

*****      *****      *      *      *      *      *      *      *      *      *      *
SEQ ID NO:10 MQDPNKSRLDPVYYRCNTDPHHRVGSKYKVYPTYDFACPFVDALEGVTHALRSSEYHDRN
GI:3435196 MQDPNKA MRDPVYYRCNPMSHHRIGDKYKIYPTYDFACPFVDSLEGITHALRSSEYHDRN

***      *      *      *      *      *      *      *      *      *      *      *      *
SEQ ID NO:10 AQYYRILQDMGLRRVEIYEFSLNMVYTLLSKRKLLWFVQNKVEDWTDPRFPTVQGIVR
GI:3435196 AQYFKVLEDMGLRQVQLYEFSLNLVFTLLSKRKLLWFVQTGLVDGWDDPRFPTVQGIVR

*****      *****      *      *      *      *      *      *      *      *      *      *
SEQ ID NO:10 RGLKVEALIQFILQQGASKNLNLMEWDKLWTINKKIIDPVCARHTAVLKDQRVIFTLTNG
GI:3435196 RGLKIEALIQFILEQQGASKNLNLMEWDKLWSINKRIIDPVCPRHTAVVAERRVLFTLTDG

*      *      *      *      *      *      *      *      *      *      *      *      *
SEQ ID NO:10 PEEPFVRILPRHKKFEGAGKKATTFANRIWLDYADAAAINKGEEVTLMDWGNAIVKEI-K
GI:3435196 PDEPFVRMIPKHKKFEGAGEKATTFTKSIWLEEADASAIVGEEVTLMDWGNAIVKEITK

*      *      *      *      *      *      *      *      *      *      *      *      *
SEQ ID NO:10 VESGVITELVGELHLEGSVKTTKLKITWLADIEELVPLSVEFDYLISKKKLEEDEDFLD
GI:3435196 DEEGRVTALSGVNLQGSVKTTKLTLWPDTNELVNLTLTEFDYLITKKLEDDDEVAD

*      *      *      *      *      *      *      *      *      *      *      *      *
SEQ ID NO:10 NLNPCTRREIPALGDANMRNIKRGEIIQLERKGYYRCDAFPFIRSSKPVVLFAIPDGRQQA

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GI:3435196 FVNPNTKKETLALGDSNMRNLKGDVILERKGYFRCDVPFKSSKPIVLFSIPDGAA-

SEQ ID NO:10 SLS
GI:3435196 --K